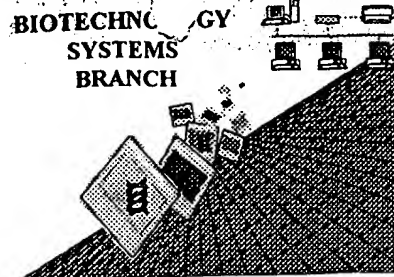


## **RAW SEQUENCE LISTING** **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/770,517  
Source: OIPE  
Date Processed by STIC: 7/25/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/770,517
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

AMC/MH - Biotechnology Systems Branch - 08/21/2001

Field 220 must be blank.

Field 221 must include a term from the name/key table 5 or 6

Field 222 must specify a location in the nucleic acid sequence

Field 223 must include ~~values of~~ description of n and any other description in your own words up to 4 lines of text.

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/770,517

DATE: 07/25/2001

TIME: 13:48:46

Input Set : A:\06501-072001.txt

Output Set: N:\CRF3\07252001\I770517.raw

Does Not Comply  
Corrected Diskette Needed

4 <110> APPLICANT: Mitsuhashi, Kazuya  
 5 Yamamoto, Hiroaki  
 6 Matsuyama, Akinobu  
 7 Tokuyama, Shinji  
 9 <120> TITLE OF INVENTION: D-AMINOACYLASE AND GENE ENCODING THE SAME  
 11 <130> FILE REFERENCE: 06501-072001  
 13 <140> CURRENT APPLICATION NUMBER: US 09/770,517  
 14 <141> CURRENT FILING DATE: 2001-01-26  
 16 <150> PRIOR APPLICATION NUMBER: JP 2000-019080  
 17 <151> PRIOR FILING DATE: 2000-01-27  
 19 <150> PRIOR APPLICATION NUMBER: JP 2000-150578  
 20 <151> PRIOR FILING DATE: 2000-05-22  
 22 <160> NUMBER OF SEQ ID NOS: 27  
 24 <170> SOFTWARE: PatentIn Ver. 2.0  
 26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 1677  
 28 <212> TYPE: DNA  
 29 <213> ORGANISM: Hypomyces mycophilus  
 31 <400> SEQUENCE: 1  
 32 atgcggaactg aaattctctt ccaactcagcc actgttatca ccggcgatga agcagcccag 60  
 33 ccctttgtgg ccgatgtgct ggtttcgaag ggactgattg ccaagattgg taaccccgg 120  
 34 tccatcaatg caactccaga tacgcggcat ctgcagctca caggctacat tctatctcct 180  
 35 ggtttcatcg atatgcatgc gcattcagac ctctacctac tctctcatcc tgaccacgag 240  
 36 gccaaaatca cccaaggatg cacaacggaa gttgtggggc aagacgggat atcatatgca 300  
 37 ccaattcgta atgtagacca gttgagggcg atccgagaac agattgctgg atggaatggc 360  
 38 aatcctacag atgaggagtg ccggacaact ctcaaaggcg ttggcatggt tgaatggcag 420  
 39 actattgggg aatacttggg ttgtttggag agaaacagga cggccactaa tgtcgccatg 480  
 40 ttggttccgc aaggcaacct gagattattg gcattgtggc catacgatac tccagcatct 540  
 41 gcagaagaga ttcaagatca aatccagctc ttgcgagagg ctatggctca ggggtgctgc 600  
 42 gggatgtcta gtggtctcac ttatacacc ccggcatgatg cttccacgtc ggaactagct 660  
 43 tctctgtgcg cgccctcgc acaagaattt ccagggtgat tctatgcgcc acatcataga 720  
 44 agttatgggt tccaggccat cgaaagtatt gccgaaatgt tggatctcgg agagtcaaca 780  
 45 ggctgtccca ttcatcttac acatgcaacg ctcaactttt cagaaaataa gggtaaagct 840  
 46 cctgtctctc tctctatggt tgataaatct cttgctgcag gcgtggatgt cacacttgat 900  
 47 acgtatccat acttgccagg ctgtacaact ctggctgcat tgttgccaag ttgggcatct 960  
 48 gctggcggcc cacaagagac gcttaaaagg cttgaggatg cagaatcgag agaaaagatt 1020  
 49 cgtatagccg tggaaatcaa aggtgtgat ggccggccatg gtattccaac caactgggac 1080  
 50 gaaatccaga tcgggacgac taatgaacca tcaatcgcat cgtattctgg tcgcaggcta 1140  
 51 tcagaagtgg cacagtctgt tggaaagccg accatogaag tctttttcga gattctgcaa 1200  
 52 aaggataagc tcgcaacgag ctgtatcatg catgttggca atgaagaaaa cgtccgacag 1260  
 53 atcatgcagc atcgggtcca tatggcaggc agtgatggga tcttgcacgg gcagacgcta 1320  
 54 caccacgag cttatggcac attcacgagg actattctcg tgaactctcg 1380  
 55 cttgttgctc tgccgtccat gatcgctcac cttacatcac ggccgcgcaa acgactttcg 1440  
 56 gtatatccat atcgcggtct gattgctgaa ggatccgctg ccgacattgt ggtttttaac 1500  
 57 ccggaacg taaaggatat gtcgacgtat gaagagccaa aggtgccaag tcggggcatt 1560  
 58 agatttgttc tagttaacgg ccagatagct gtggacgaag gcaagatgac aggcacaaga 1620  
 59 gggggtaaaa cactgagaag aagcaccgat ggcaaggatg aggcagaaga tgagtaa 1677

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/770,517

DATE: 07/25/2001

TIME: 13:48:46

Input Set : A:\06501-072001.txt

Output Set: N:\CRF3\07252001\I770517.raw

```

61 <210> SEQ ID NO: 2
62 <211> LENGTH: 558
63 <212> TYPE: PRT
64 <213> ORGANISM: Hypomyces mycophilus
66 <400> SEQUENCE: 2
67 Met Arg Thr Glu Ile Leu Phe His Ser Ala Thr Val Ile Thr Gly Asp
68   1           5           10           15
69 Glu Ala Ala Gln Pro Phe Val Ala Asp Val Leu Val Ser Lys Gly Leu
70           20           25           30
71 Ile Ala Lys Ile Gly Asn Pro Gly Ser Ile Asn Ala Thr Pro Asp Thr
72           35           40           45
73 Arg His Leu Asp Val Thr Gly Tyr Ile Leu Ser Pro Gly Phe Ile Asp
74           50           55           60
75 Met His Ala His Ser Asp Leu Tyr Leu Leu Ser His Pro Asp His Glu
76   65           70           75           80
77 Ala Lys Ile Thr Gln Gly Cys Thr Thr Glu Val Val Gly Gln Asp Gly
78           85           90           95
79 Ile Ser Tyr Ala Pro Ile Arg Asn Val Asp Gln Leu Arg Ala Ile Arg
80           100          105          110
81 Glu Gln Ile Ala Gly Trp Asn Gly Asn Pro Thr Asp Glu Glu Cys Arg
82           115          120          125
83 Thr Thr Leu Lys Gly Val Gly Met Phe Glu Trp Gln Thr Ile Gly Glu
84           130          135          140
85 Tyr Leu Asp Cys Leu Glu Arg Asn Arg Thr Ala Thr Asn Val Ala Met
86 145          150          155          160
87 Leu Val Pro Gln Gly Asn Leu Arg Leu Leu Ala Cys Gly Pro Tyr Asp
88           165          170          175
89 Thr Pro Ala Ser Ala Glu Glu Ile Gln Asp Gln Ile Gln Leu Leu Arg
90           180          185          190
91 Glu Ala Met Ala Gln Gly Ala Val Gly Met Ser Ser Gly Leu Thr Tyr
92           195          200          205
93 Thr Pro Gly Met Tyr Ala Ser Thr Ser Glu Leu Ala Ser Leu Cys Ala
94           210          215          220
95 Ala Leu Ala Gln Glu Phe Pro Gly Ala Phe Tyr Ala Pro His His Arg
96 225          230          235          240
97 Ser Tyr Gly Phe Gln Ala Ile Glu Ser Tyr Ala Glu Met Leu Asp Leu
98           245          250          255
99 Gly Glu Ser Thr Gly Cys Pro Ile His Leu Thr His Ala Thr Leu Asn
100          260          265          270
101 Phe Ser Glu Asn Lys Gly Lys Ala Pro Val Leu Ile Ser Met Val Asp
102          275          280          285
103 Lys Ser Leu Ala Ala Gly Val Asp Val Thr Leu Asp Thr Tyr Pro Tyr
104          290          295          300
105 Leu Pro Gly Cys Thr Thr Leu Ala Ala Leu Leu Pro Ser Trp Ala Ser
106 305          310          315          320
107 Ala Gly Gly Pro Gln Glu Thr Leu Lys Arg Leu Glu Asp Ala Glu Ser
108           325          330          335
109 Arg Glu Lys Ile Arg Ile Ala Val Glu Ile Lys Gly Cys Asp Gly Gly
110          340          345          350

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/770,517

DATE: 07/25/2001

TIME: 13:48:46

Input Set : A:\06501-072001.txt

Output Set: N:\CRF3\07252001\I770517.raw

```

111 His Gly Ile Pro Thr Asn Trp Asp Glu Ile Gln Ile Gly Thr Thr Asn
112          355                      360                      365
113 Glu Pro Ser Ile Ala Ser Tyr Ser Gly Arg Arg Leu Ser Glu Val Ala
114          370                      375                      380
115 Gln Ser Val Gly Lys Pro Thr Ile Glu Val Phe Phe Glu Ile Leu Gln
116 385                      390                      395                      400
117 Lys Asp Lys Leu Ala Thr Ser Cys Ile Met His Val Gly Asn Glu Glu
118                      405                      410                      415
119 Asn Val Arg Gln Ile Met Gln His Arg Val His Met Ala Gly Ser Asp
120                      420                      425                      430
121 Gly Ile Leu His Gly Gln Thr Leu His Pro Arg Ala Tyr Gly Thr Phe
122          435                      440                      445
123 Thr Arg Tyr Leu Gly His Tyr Ser Arg Glu Leu Ser Leu Val Ala Leu
124          450                      455                      460
125 Pro Ser Met Ile Ala His Leu Thr Ser Arg Pro Ala Lys Arg Leu Ser
126 465                      470                      475                      480
127 Val Tyr Pro Tyr Arg Gly Leu Ile Ala Glu Gly Ser Ala Ala Asp Ile
128                      485                      490                      495
129 Val Val Phe Asn Pro Glu Thr Val Lys Asp Met Ser Thr Tyr Glu Glu
130                      500                      505                      510
131 Pro Lys Val Pro Ser Arg Gly Ile Arg Phe Val Leu Val Asn Gly Gln
132          515                      520                      525
133 Ile Ala Val Asp Glu Gly Lys Met Thr Gly Thr Arg Gly Gly Lys Thr
134          530                      535                      540
135 Leu Arg Arg Ser Thr Asp Gly Lys Val Lys Ala Arg Asp Glu
136 545                      550                      555

```

138 &lt;210&gt; SEQ ID NO: 3

139 &lt;211&gt; LENGTH: 20

140 &lt;212&gt; TYPE: DNA

141 &lt;213&gt; ORGANISM: Artificial Sequence

143 &lt;220&gt; FEATURE:

144 &lt;223&gt; OTHER INFORMATION: Artificially Synthesized Primer Sequence

146 &lt;400&gt; SEQUENCE: 3

147 cccggcttca tcgacatgca

20

149 &lt;210&gt; SEQ ID NO: 4

150 &lt;211&gt; LENGTH: 20

151 &lt;212&gt; TYPE: DNA

152 &lt;213&gt; ORGANISM: Artificial Sequence

W--&gt; 154 &lt;220&gt; FEATURE: misc. feature

W--&gt; 155 &lt;221&gt; NAME/KEY: (18)

W--&gt; 156 n is A,T,C, or G

158 &lt;223&gt; OTHER INFORMATION: Artificially Synthesized Primer Sequence

160 &lt;400&gt; SEQUENCE: 4

W--&gt; 161 ttcatcgaca tgcaygcna

163 &lt;210&gt; SEQ ID NO: 5

164 &lt;211&gt; LENGTH: 20

165 &lt;212&gt; TYPE: DNA

166 &lt;213&gt; ORGANISM: Artificial Sequence

W--&gt; 168 &lt;220&gt; FEATURE: misc. feature

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/770,517

DATE: 07/25/2001  
TIME: 13:48:46

Input Set : A:\06501-072001.txt  
Output Set: N:\CRF3\07252001\I770517.raw

```

W--> 169 <221> NAME/KEY: (3, 6, 15)
W--> 170      n is A,T,C, or G
      172 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
      174 <400> SEQUENCE: 5
W--> 175 tgnggngcrt craangcytg 20
      177 <210> SEQ ID NO: 6
      178 <211> LENGTH: 20
      179 <212> TYPE: DNA
      180 <213> ORGANISM: Artificial Sequence
W--> 182 <220> FEATURE: misc. feature
W--> 183 <221> NAME/KEY: (3, 9)
W--> 184      n is A,T,C, or G
      186 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
      188 <400> SEQUENCE: 6
W--> 189 aangcytgng grtaytcrtc 20
      191 <210> SEQ ID NO: 7
      192 <211> LENGTH: 321
      193 <212> TYPE: DNA
      194 <213> ORGANISM: Hypomyces mycophilus
      196 <400> SEQUENCE: 7
      197 ttcacgcaca tgcacgcgca gctggatggt caaccttgac aactacaaca agatactctc 60
      198 tgtagacaaa aaatcggggg tegtggatcat gcagagcggc attcgactat acaccctttg 120
      199 cgaagagctg gagctacatg gcctggcaat gccgaacctg ggcagtataa acgagcaatc 180
      200 catcgccggc gccatatcta caggcacaca cggcagcagc atccaccacg gcctcatgtc 240
      201 tgaggatatt ctgcctctga aaatcaactct cgcggggcggc aagacggagg catgctccaa 300
      202 agacgaatac ccccaagcct t 321
      204 <210> SEQ ID NO: 8
      205 <211> LENGTH: 20
      206 <212> TYPE: DNA
      207 <213> ORGANISM: Artificial Sequence
      209 <220> FEATURE:
      210 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
      212 <400> SEQUENCE: 8
      213 aggccaaaat caccgaagga 20
      215 <210> SEQ ID NO: 9
      216 <211> LENGTH: 20
      217 <212> TYPE: DNA
      218 <213> ORGANISM: Artificial Sequence
      220 <220> FEATURE:
      221 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
      223 <400> SEQUENCE: 9
      224 attggggaat acttggttg 20
      226 <210> SEQ ID NO: 10
      227 <211> LENGTH: 20
      228 <212> TYPE: DNA
      229 <213> ORGANISM: Artificial Sequence
      231 <220> FEATURE:
      232 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
      234 <400> SEQUENCE: 10

```

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/770,517

DATE: 07/25/2001  
TIME: 13:48:46

Input Set : A:\06501-072001.txt  
Output Set: N:\CRF3\07252001\I770517.raw

```

235 ctgggtcttt ccgcctcaga                                20
237 <210> SEQ ID NO: 11
238 <211> LENGTH: 20
239 <212> TYPE: DNA
240 <213> ORGANISM: Artificial Sequence
242 <220> FEATURE:
243 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
245 <400> SEQUENCE: 11
246 attaacccctc actaaagggc                                20
248 <210> SEQ ID NO: 12
249 <211> LENGTH: 1325
250 <212> TYPE: DNA
251 <213> ORGANISM: Hypomyces mycophilus
253 <400> SEQUENCE: 12
254 caggacggcc actaatgtcg ccatgttggg tccgcaaggc aacctgagat tattggcatg    60
255 tggcccatac gatactccag catctgcaga agagattcaa gatcaaattc agctcttgcg    120
256 agaggctatg gctcagggtg ctgtcgggat gtctagtggg ctcaattata caccggcgat    180
257 gtatgcttcc acgtcggaac tagcttctct gtgcgcggcc ctgcacaaag aatttcaggg    240
258 tgcattctat gcgccacatc atagaagtta tgggttcag gccatcgaaa gttatgccga    300
259 aatgttggat ctcgagagat caacaggctg tccattcat cttacacatg caacgctcaa    360
260 cttttcagaa aataagggta aagctcctgt cctcatctct atggttgata aatctcttgc    420
261 tgcaggcgtg gatgtcacac ttgatacgta tccatacttg ccaggctgta caactctggc    480
262 tgcattgctg ccaagtcggg catctgctgg cggcccacaa gagacgctta aaaggcttga    540
263 ggatgcagaa tcgagagaaa agattcgtat agccgtggaa atcaaagggt gtgatggcgg    600
264 ccatggtatt ccaaccaact gggacgaaat ccagatcggg acgactaatg aaccatcaat    660
265 cgcctcgtat tctggtcgca ggctatcaga agtggcacag tctgttgtaa agccgaccat    720
266 cgaagtcttt ttcgagattc tgcaaaaagg taagctcgca acgagctgta tcatgcatgt    780
267 tggcaatgaa gaaaacgtcc gacagatcat gcagcatcgg gtccatattg caggcagtga    840
268 tgggatcttg cactggcgca cgctacaccc acgagcttat ggcacattca cgcggtattt    900
269 aggacactat tctcgtgaac tctcgttgtt tgcctgcgg tccatgatcg ctacacctac    960
270 atcacggccc gccaaacgac ttctcgtata tccatatcgc ggtctgattg ctgaaggatc   1020
271 cgctgcgcac attgtggttt ttaaccccga aacggtaaag gatatgtcga cgtatgaaga   1080
272 gccaaagggt ccaagtcggg gcattagatt tgttctagtt aacggccaga tagctgtgga   1140
273 cgaaggcaag atgacaggca caagaggggg taaaacactg agaagaagca ccgatggcaa   1200
274 ggtgaaggca agagatgagt aaagtctcga tctgcatccg cgtgcccac aacaggatca   1260
275 agtcgtcaca gcatgatacg gcaggctttg gagtagatac catgtcatgg gggaaatggt   1320
276 caata                                                1325
278 <210> SEQ ID NO: 13
279 <211> LENGTH: 21
280 <212> TYPE: DNA
281 <213> ORGANISM: Artificial Sequence
283 <220> FEATURE:
284 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
286 <400> SEQUENCE: 13
287 cggagagtca acaggctgtc c                                21
289 <210> SEQ ID NO: 14
290 <211> LENGTH: 20
291 <212> TYPE: DNA
292 <213> ORGANISM: Artificial Sequence

```

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/770,517

DATE: 07/25/2001

TIME: 13:48:47

Input Set : A:\06501-072001.txt

Output Set: N:\CRF3\07252001\I770517.raw

L:154 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:155 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4  
L:156 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:4  
L:161 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4  
L:161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:168 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:169 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:170 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:5  
L:175 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:182 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:183 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6  
L:184 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:6  
L:189 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6  
L:189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6



**STATISTICS SUMMARY**

PATENT APPLICATION: US/09/770,517

DATE: 07/25/2001

TIME: 13:48:47

Input Set : A:\06501-072001.txt

Output Set: N:\CRF3\07252001\I770517.raw

Application Serial Number: US/09/770,517

Alpha or Numeric: Numeric

Application Class:

Application File Date: 01-26-2001

Art Unit: OIPE

Software Application: PatentIn

Total Number of Sequences: 27

Total Nucleotides: 5900

Total Amino Acids: 603

Number of Errors: 0

Number of Warnings: 15

Number of Corrections: 0

**MESSAGE SUMMARY**

256 W: 3 (Invalid Numeric Header Field)

257 W: 6 (Feature value mis-spelled or invalid)

258 W: 3 (Mandatory Feature missing)

341 W: 3 ((46) "n" or "Xaa" used)